Molecular Characterization of *Mycobacterium abscessus* Strains Isolated from a Hospital Outbreak

To the Editor: In recent years there have been several reports of sporadic and epidemic hospital-acquired infections caused by rapidly growing mycobacteria, namely, *Mycobacterium abscessus*, *M. chelonae,* and *M. fortuitum*. *M. abscessus* has been well documented as a cause of cutaneous and soft tissue infections and has been implicated in chronic ear infections, bacteremia associated with hemodialysis equipment, and peritoneal dialysis–related infections (1).

Differentiating mycobacteria to the species level is difficult because of the diversity of available techniques and the time required for full identification. A rapid method based on the evaluation of the gene coding for the 65-kDa heat shock protein, which contains epitopes both unique and common to various species of mycobacteria, has been reported (2). A 383-bp sequence situated at the amino terminus of this 65-kDa antigen (3) has been shown to be conserved among several species of mycobacteria. Reports based on polymerase chain reaction (PCR) amplification and DNA sequencing (4) show species-specific polymorphism at the nucleotide level within this region (5). The conserved nature of this gene allows differentiation of mycobacteria within 1 day by restriction enzyme digestion of PCR products obtained by using primers common to all mycobacteria.

From August through December 1995, postoperative wound infections developed in 45 patients in the pediatric surgery unit of Kalawati Saran Children's Hospital, New Delhi, India; 42 were day-care patients, and 3 were inpatients who had undergone major surgery. Thirty-two clinical samples (pus and exudate) were tested for acid-fast bacilli by the Ziehl-Neelson method; the same smear samples were cultured on Lowenstein-Jensen slants and examined for growth daily for 4 days and thereafter twice a week for 8 weeks. The

organism was identified biochemically (i.e., by the niacin and nitrate production test) as *M. abscessus*.

The genomic DNA from the culture of mycobacterial isolates was extracted by standardized protocol (6) and subjected to PCR-restriction enzyme pattern analysis (PRA) (2). Primers TB11 (5'-ACC AAC GAT GGG GTG TGT CCA T) and TB12 (5'-CTT GTC GAA CCG CAT ACC CT) amplified a 439-bp fragment between positions 398 and 836 of the published gene sequence for 65-kDa heat shock protein (3). The PCR products were then digested separately by using restriction enzymes *Bst* EII and *Hae*III. The digests were fractionated on nondenaturing 10% polyacrylamide gel. The *Bst* EII pattern generated during PRA yielded two 235/210-bp bands similar to the patterns attributed to *M. chelonae* subsp. *abscessus* (2). The patterns displayed on *Hae*III digestion had distinctive 150/60-bp bands that were once again similar to the pattern attributed to *M. chelonae* subsp. *abscessus* (2). PRA results confirmed that the isolates were *M. abscessus*. The source of the outbreak was traced to the tap water in the operating room and to a defective autoclaving process (the result of a leaking vacuum pump and faulty pressure gauge in the autoclave).

This report highlights the role of rapidly growing mycobacteria in a water-related nosocomial outbreak. The PCR-PRA method promises to be a very rapid, economical, and universal system of identifying mycobacteria to the species level. This technique does not require hybridization to a panel of species-specific probes, which is a limitation of other PCR-based and hybridization methods for differentiating mycobacterial species. This method has the potential to be a useful diagnostic as well as epidemiologic marker for typing isolates of most mycobacteria during institutional outbreaks.

Lakshmy Anantha Raman,* Noman Siddiqi, †‡ Mohammed Shamim,† Monorama Deb,* Geeta Mehta,* and Seyed Ehtesham Hasnain†‡
*Lady Hardinge Medical College, New Delhi, India; †National Institute of Immunology, New Delhi, India; ‡Centre for DNA Fingerprinting and Diagnostics, Hyderabad, India

References

1. Hakim A, Hisam N, Reuman PD. Environmental mycobacterial peritonitis complicating peritoneal dialysis: three cases and review. Clin Infect Dis 1993;16:426-31.
2. Telenti A, Marchesi F, Balz M, Baally F, Bottger EC, Bodmer T. Rapid identification of Mycobacteria to the species level by polymerase chain reaction and restriction enzyme analysis. J Clin Microbiol 1993;31:175-8.
3. Shinnick T. The 65-kilodalton antigen of *Mycobacterium tuberculosis*. J Bacteriol 1987;169:1080-8.
4. Brisson-Noel A, Aznar C, Chureau C, Nguyen S, Pierre C, Bartoli M, et al. Diagnosis of tuberculosis by DNA amplification in clinical practice evaluation. Lancet 1991;338:364-6.
5. Hance A, Grandchamp B, Levy-Frebaault V, Lecossier D, Rauzier JJ, Bocart D, et al. Detection and identification of mycobacteria by amplification of mycobacterial DNA. Mol Microbiol 1989;3:843-9.
6. Siddiqi N, Shamim M, Jain NK, Rattan A, Amin A, Katoch VM, et al. Molecular anaylsis of multi-drug resistance in Indian isolates of *Mycobacterium tuberculosis*. Mem Inst Oswaldo Cruz 1998;3:589-94.